SEQUENCE LISTING

<110> Newell, Martha K.

<120> Methods and Products for Manipulating
Uncoupling Protein Expression in the Plasma Membrane

<130> I0277/7009

<150> US 60/140,574
<151> 1999-06-23

<160> 6

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 924
<212> DNA
<213> Homo sapiens

<400> 1

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acaatcaccg ctgtggtaaa aacagaaggg cggatgaaac tctacagcgg gctgcctgcg  240
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cttcaagcac agagccatct ccacggaatc aaacctcgct acacggggac ttataatgcg  480
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aacgaaggac caacggcttt cttcaagggg ttggtacctt ccttcttgcg acttggatcc  840
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<210> 2
<211> 307
<212> PRT
<213> Homo sapiens

<400> 2

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Leu Phe Ser Ala Gly Ile Ala Ala Cys Leu Ala Asp Val Ile Thr Phe
            20                  25                  30
Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Val Gln Gly Glu Cys Pro
        35                  40                  45
Thr Ser Ser Val Ile Arg Tyr Lys Gly Val Leu Gly Thr Ile Thr Ala
    50                  55                  60
Val Val Lys Thr Glu Gly Arg Met Lys Leu Tyr Ser Gly Leu Pro Ala
65                  70                  75                  80
Gly Leu Gln Arg Gln Ile Ser Ser Ala Ser Leu Arg Ile Gly Leu Tyr
                85                  90                  95
Asp Thr Val Gln Glu Phe Leu Thr Ala Gly Lys Glu Thr Ala Pro Ser
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                100                 105                 110
Leu Gly Ser Lys Ile Leu Ala Gly Leu Thr Thr Gly Gly Val Ala Val
            115                 120                 125
Phe Ile Gly Gln Pro Thr Glu Val Val Lys Val Arg Leu Gln Ala Gln
    130                 135                 140
Ser His Leu His Gly Ile Lys Pro Arg Tyr Thr Gly Thr Tyr Asn Ala
145                 150                 155                 160
Tyr Arg Ile Ile Ala Thr Thr Glu Gly Leu Thr Gly Leu Trp Lys Gly
                165                 170                 175
Thr Thr Pro Asn Leu Met Arg Ser Val Ile Ile Asn Cys Thr Glu Leu
            180                 185                 190
Val Thr Tyr Asp Leu Met Lys Glu Ala Phe Val Lys Asn Asn Ile Leu
        195                 200                 205
Ala Asp Asp Val Pro Cys His Leu Val Ser Ala Leu Ile Ala Gly Phe
    210                 215                 220
Cys Ala Thr Ala Met Ser Ser Pro Val Asp Val Val Lys Thr Arg Phe
225                 230                 235                 240
Ile Asn Ser Pro Pro Gly Gln Tyr Lys Ser Val Pro Asn Cys Ala Met
                245                 250                 255
Lys Val Phe Thr Asn Glu Gly Pro Thr Ala Phe Phe Lys Gly Leu Val
            260                 265                 270
Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Ile Met Phe Val Cys
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Phe Glu Gln Leu Lys Arg Glu Leu Ser Lys Ser Arg Gln Thr Met Asp
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Cys Ala Thr
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<210> 3
<211> 1105
<212> DNA
<213> Homo sapiens

<400> 3

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tactgccact gtgaagtttc ttggggctgg cacagctgcc tgcatcgcag atctcatcac    180
ctttcctctg gatactgcta aagtccggtt acagatccaa ggagaaagtc aggggccagt    240
gcgcgctaca gccagcgccc agtaccgcgg tgtgatgggc accattctga ccatggtgcg    300
tactgagggc ccccgaagcc tctacaatgg gctggttgcc ggcctgcagc gccaaatgag    360
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tgagcatgcc agcattggga gccgcctcct agcaggcagc accacaggtg ccctggctgt    480
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agggttcatg ccctcctttc tccgcttggg ttcctggaac gtggtgatgt tcgtcaccta    960
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ctctcctgct gctgacctga tcacctctgg ctttgtctct agccgggcca tgctttcctt   1080
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<210> 4
<211> 309
<212> PRT
<213> Homo sapiens

<400> 4

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            20                  25                  30
Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln
        35                  40                  45
Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr Arg Gly Val Met Gly
    50                  55                  60
Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn
65                  70                  75                  80
Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg
                85                  90                  95
Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu
            100                 105                 110
His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly Ser Thr Thr Gly Ala
        115                 120                 125
Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
    130                 135                 140
Gln Ala Gln Ala Arg Ala Gly Gly Gly Arg Arg Tyr Gln Ser Thr Val
145                 150                 155                 160
Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp
                165                 170                 175
Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala
            180                 185                 190
Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn
        195                 200                 205
Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala
    210                 215                 220
Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr
225                 230                 235                 240
Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys
                245                 250                 255
Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly
            260                 265                 270
Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe
        275                 280                 285
Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Ala Ala Cys Thr Ser
    290                 295                 300
Arg Glu Ala Pro Phe
305
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<210> 5
<211> 1132
<212> DNA
<213> Homo sapiens

<400> 5

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gttacctttc cactggacac agccaaggtc cgcctgcaga tccaggggga gaaccaggcg     300
gtccagacgg cccggctcgt gcagtaccgt ggcgtgctgg gcaccatcct gaccatggtg     360
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ggcgcggaca actccagcct cactacccgg attttggccg gctgcaccac aggagccatg     540
gcggtgacct gtgcccagcc cacagatgtg gtgaaggtcc gatttcaggc cagcatacac     600
ctcgggccat ccaggagcga cagaaaatac agcgggacta tggacgccta cagaaccatc     660
gccagggagg aaggagtcag gggcctgtgg aaaggaactt tgcccaacat catgaggaat     720
gctatcgtca actgtgctga ggtggtgacc tacgacatcc tcaaggagaa gctgctggac     780
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ccaggccagt acttcagccc cctcgactgt atgataaaga tggtggccca ggagggcccc 960
acagccttct acaaggggtg agcctcctcc tgcctccagc actcctccc agagaacagg 1020
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<210> 6
<211> 275
<212> PRT
<213> Homo sapiens

<400> 6

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Phe Leu Gly Ala Gly Thr Ala Ala Cys Phe Ala Asp Leu Val Thr Phe
20 25 30
Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Asn Gln
35 40 45
Ala Val Gln Thr Ala Arg Leu Val Gln Tyr Arg Gly Val Leu Gly Thr
50 55 60
Ile Leu Thr Met Val Arg Thr Glu Gly Pro Cys Ser Pro Tyr Asn Gly
65 70 75 80
Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Ile Arg Ile
85 90 95
Gly Leu Tyr Asp Ser Val Lys Gln Val Tyr Thr Pro Lys Gly Ala Asp
100 105 110
Asn Ser Ser Leu Thr Thr Arg Ile Leu Ala Gly Cys Thr Thr Gly Ala
115 120 125
Met Ala Val Thr Cys Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
130 135 140
Gln Ala Ser Ile His Leu Gly Pro Ser Arg Ser Asp Arg Lys Tyr Ser
145 150 155 160
Gly Thr Met Asp Ala Tyr Arg Thr Ile Ala Arg Glu Glu Gly Val Arg
165 170 175
Gly Leu Trp Lys Gly Thr Leu Pro Asn Ile Met Arg Asn Ala Ile Val
180 185 190
Asn Cys Ala Glu Val Val Thr Tyr Asp Ile Leu Lys Glu Lys Leu Leu
195 200 205
Asp Tyr His Leu Leu Thr Asp Asn Phe Pro Cys His Phe Val Ser Ala
210 215 220
Phe Gly Ala Gly Phe Cys Ala Thr Val Val Ala Ser Pro Val Asp Val
225 230 235 240
Val Lys Thr Arg Tyr Met Asn Ser Pro Pro Gly Gln Tyr Phe Ser Pro
245 250 255
Leu Asp Cys Met Ile Lys Met Val Ala Gln Glu Gly Pro Thr Ala Phe
260 265 270
Tyr Lys Gly
275